

Plant Genomics

Code: 43865
ECTS Credits: 6

Degree	Type	Year	Semester
4316231 Plant Biology, Genomics and Biotechnology	OB	0	1

The proposed teaching and assessment methodology that appear in the guide may be subject to changes as a result of the restrictions to face-to-face class attendance imposed by the health authorities.

Contact

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Use of Languages

Principal working language: english (eng)

Teachers

Jordi García Mas
Maria Jose Aranzana Civit
Pere Arus
Werner Howad
Raul Castanera Andres
Albert Ferrer Prats
Cristina Roquet Ruíz

External teachers

Riccardo Aiese

Prerequisites

Good command of English
Good background in genetics, molecular biology and genetic engineering

Objectives and Contextualisation

Provide a global and updated view of the theoretical and technological bases related to the study of the organization, function and evolution of plant genomes and their potential applications to the genetic improvement of crop plants.

Competences

- Apply knowledge of functional mechanisms of various different organizational levels in plants to the characterization of growth and development processes of the whole plant organism.
- Apply knowledge of plant molecular genetics in different scientific and industrial areas.

- Communicate and justify conclusions clearly and unambiguously to both specialised and non-specialised audiences.
- Continue the learning process, to a large extent autonomously.
- Develop critical reasoning in the area of study and in relation to the scientific and business environment.
- Identify and use Bio-Computer Science tools to be applied to the genetic, evolutionary and functional study of plants.
- Integrate knowledge and use it to make judgements in complex situations, with incomplete information, while keeping in mind social and ethical responsibilities.
- Solve problems in new or little-known situations within broader (or multidisciplinary) contexts related to the field of study.
- Synthesize, and analyze alternatives and debate critically.
- Use and manage bibliographical information and computer resources in the area of study.
- Use scientific terminology to argue the results of research and present them in English both orally and in writing in an international environment.
- Work in a multidisciplinary team.

Learning Outcomes

1. "Apply ""omic""-type approaches to the identification of new genes and processes of interest in basic and applied research."
2. Apply bioinformatic tools to the study of plant systems and phylogeny.
3. Apply genome sequencing and annotation strategies.
4. Apply knowledge acquired when identifying the function of new genes in basic and applied research.
5. Apply knowledge of plant genomics to the study of the evolutionary mechanisms and the systems of plants and fungi.
6. Choose and apply bioinformatic tools to genomics studies.
7. Communicate and justify conclusions clearly and unambiguously to both specialised and non-specialised audiences.
8. Continue the learning process, to a large extent autonomously.
9. Describe the organisation and function of plant genomes.
10. Develop critical reasoning in the area of study and in relation to the scientific and business environment.
11. Integrate knowledge and use it to make judgements in complex situations, with incomplete information, while keeping in mind social and ethical responsibilities.
12. Solve problems in new or little-known situations within broader (or multidisciplinary) contexts related to the field of study.
13. Synthesize, and analyze alternatives and debate critically.
14. Use and manage bibliographical information and computer resources in the area of study.
15. Use scientific terminology to argue the results of research and present them in English both orally and in writing in an international environment.
16. Work in a multidisciplinary team.

Content

- Plant genome organization and function.
- Genome sequencing strategies and annotation.
- Bioinformatics tools applied to genomic studies.
- Molecular evolution of plants.
- Genetic markers and molecular breeding.
- Transcript analysis and function.

"*Unless the requirements enforced by the health authorities demand a prioritization or reduction of these contents."

Methodology

- Lectures covering the different topics of the program. *Powerpoint* presentations will be available, in advance, at the *Campus Virtual UAB*.
- Reading of selected research papers for presentation and discussion in the seminar sessions.
- Practical sessions on bioinformatics tools applied to genomic studies
- Visit to the *National Center for Genomic Analysis (CNAG-CRG)* at the *Barcelona Science Park*.

"*The proposed teaching methodology may experience some modifications depending on the restrictions to face-to-face activities enforced by health authorities."

Annotation: Within the schedule set by the centre or degree programme, 15 minutes of one class will be reserved for students to evaluate their lecturers and their courses or modules through questionnaires.

Activities

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Bioinformatic sessions	10	0.4	1, 2, 5, 3, 12, 6, 16, 14
Classroom practices	4	0.16	1, 3, 12, 6, 14
External visit	4	0.16	1, 4, 3, 6, 14
Lectures	17	0.68	1, 2, 5, 4, 3, 9, 10, 11, 6, 14
Seminars	4	0.16	5, 10, 11, 12, 7, 13, 16, 15
Type: Supervised			
Preparation of oral presentations	30	1.2	10, 11, 12, 7, 8, 6, 13, 14, 15
Type: Autonomous			
Student work and learning	80	3.2	10, 12, 8, 13, 16

Assessment

- Written reports (Exam and exercises on bioinformatics).
- Oral presentation and defense of seminar session.
- Attendance and participation in the classroom and seminar sessions.
- The student will be "not qualificable" when the sum of marks of the different evaluations does not reach a global minimal score of 5.0 (out of 10).

*Student's assessment may experience some modifications depending on the restrictions to face-to-face activities enforced by health authorities.

Assessment Activities

Title	Weighting	Hours	ECTS	Learning Outcomes
Attendance and participation in the classroom and seminar sessions	10%	0	0	10, 13, 16
Oral presentation and defense of the seminar	30%	0	0	11, 7, 13, 14, 15
Written reports (Exam and exercises on bioinformatics)	60%	1	0.04	1, 2, 5, 4, 3, 9, 11, 12, 7, 8, 6, 13, 15

Bibliography

Specific bibliography (books, book chapters and journal articles) and useful links related to *Plant Genomics* will be provided for the different sessions of the program.

Software

Plant Genomics, subject presentation. Sessions program, Seminars, Evaluation, CNAG-CRG visit

Organization of plant genomes. Nuclear genome. Ploidy. Coding and non-coding regions in the genome. Repetitive DNA. Gene evolution. Pseudogenes. Genomic annotation. Plastid and mitochondrial genomes. RNA editing. Interaction between genomes. Epigenomics.

Plant genome plasticity and transposable elements. Impact of transposable elements in the structure and evolution of plant genomes.

Molecular markers. Definition. Types of molecular markers. Methods to obtain molecular markers. Genotyping methods.

Genetic linkage: mapping genes and quantitative traits (QTLs).

Linkage disequilibrium and Genome-Wide Association (GWAS).

Hands on seminar/computer practical: Playing with genotyping data and map construction.

Plant phylogenetics and evolution. Plant molecular evolution. Introductory concepts on phylogenetics. Gene trees versus species trees: Homology, orthology, paralogy. Concerted evolution. Hybridization and introgression. Polyploidy. Lineage sorting or deep coalescence. Molecular markers used in plant phylogenetics and phylogenomics.

Bioinformatics tools in phylogenomic studies. Orthology assessment and multiple sequence alignment. Genetic distances and nucleotide substitution models. Phylogenetic inference. Parsimony analysis. Probabilistic Methods (Maximum Likelihood). Measurements of statistical support. Coalescent based species trees.

Coding and non-coding RNAs: types and biological functions. RNA polymerases. Roles of RNAs in protein synthesis and processing. RNAi silencing mechanisms: transcriptional and posttranscriptional. Small RNAs: siRNAs and hpRNAs. miRNAs: action, roles and applications. lncRNAs.

High throughput sequencing. Introduction to Next-Generation Sequencing platforms. Examples of applications: de novo genome sequencing, genome re-sequencing, exome sequencing, methylome sequencing.

Next-Generation Sequencing technologies for transcriptomics. Design of RNA-seq experiments. RNA-seq (Illumina) data analysis: identification of differentially expressed genes. Practical use of the AIR platform.

Visit to the "Nacional Center of Genomic Analysis" (CNAG-CRG). Overview of the CNAG. Next Generation Sequencing technologies. Bioinformatics essentials for Next Generation Sequencing. De novo assembly and annotation in plant genomes.

Seminars. Oral presentations by students.